

# SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, DNAs encoding the polypeptides, and utility of the Polypeptides

<130> Q79834

<140> 10/774,378

<141> 2004-02-10

<150> 09/380,276

<151> 1999-08-27

<150> JP 9-43143

<151> 1997-02-27

<150> PCT/JP98/00799

<151> 1997-02-27

<160> 15

<170> PatentIn version 3.0

<210> 1

<211> 1251

<212> DNA

<213> Homo Sapiens

<400> 1

atggctttaa aagtgtact agaacaagag aaaacgtttt tcactctttt agtattacta	60
ggctatttgt catgtaaagt gacttgtgaa acaggagact gtagacagca agaattcagg	120
gatcgggtctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag	180
gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggtc	240
aaggaggact ggggcttcca gaaatgcaag ccctgtctgg actgcgagc ggtgaaccgc	300
tttcagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga	360
ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac	420
cctcctcctc cttacgaacc gcactgtgcc agcaagggtca acctcgtgaa gatcgcgtcc	480
acggcctcca gcccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc	540
gtcctgctgg ccctgctcat cctctgtgtc atctattgta agagacagtt tatggagaag	600
aaaccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt	660
cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac	720
tcagtgcaga cctgcgggcc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc	780
agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga	840
aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc	900
tgtggcgagt tttcagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc	960
tctttttgtg actcttatcc tgaactcact ggagaagaca ttcattctct caatccagaa	1020

cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctggt	1080
ccagtccagt ctcatctga aaactttaca gcagctactg atttatctag atataacaac	1140
acactggtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag	1200
gagagtggcg ctatcatcca cccagccact cagacgtccc tccaggaagc t	1251

<210> 2  
 <211> 1704  
 <212> DNA  
 <213> Homo sapiens

<400> 2	
gggaacgtag aactctccaa caataaatac atttgataag aaagatggct ttaaaagtgc	60
tactagaaca agagaaaacg tttttcactc ttttagtatt actaggctat ttgtcatgta	120
aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact	180
gtgttccttg caaccagtgt gggccaggca tggagtgtgc taaggaatgt ggcttcggct	240
atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct	300
tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt	360
gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga	420
aacttgtcgg ctttcaagac atggagtgtg tgccttgtgg agaccctcct cctccttacg	480
aaccgcactg tgccagcaag gtcaacctcg tgaagatcgc gtccacggcc tccagcccac	540
gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc	600
tcacctctg tgtcatctat tgtaagagac agtttatgga gaagaaaccc agctggcttc	660
tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc	720
tccacgaata tgcccacaga gcctgctgcc agtgccgccg tgactcagtg cagacctgcg	780
ggccggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aaccggcgga	840
ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg	900
gggagatggt gccgactttc ttcggatccc tcacgcagtc catctgtggc gagttttcag	960
atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt	1020
atcctgaact cactggagaa gacattcatt ctctcaatcc agaacttgaa agctcaacgt	1080
ctttggattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt	1140
ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag	1200
catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca	1260
tccacccagc cactcagacg tccctccagg aagcttaaag aacctgcttc tttctgcagt	1320
agaagcgtgt gctggaaccc aaagagtact cctttgtag gcttatggac tgagcagtct	1380
ggaccttgca tggcttctgg ggcaaaaata aatctgaacc aaactgacgg catttgaagc	1440

```

ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa 1500
gaaaagactc caggccgact catgatactc tgcattcttc ctacatgaga agcttctctg 1560
ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat 1620
ataacaagaa acagaaatgc cctcatgctt attttcatgg tgattgtggt tttacaagac 1680
tgaagaccca gagtatactt tttc 1704

```

```

<210> 3
<211> 1704
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Origin: human bone marrow stromal cell line HAS303

```

```

<220>
<221> CDS
<222> (45)..(1295)

```

```

<220>
<221> sig_peptide
<222> (45)..(119)

```

```

<220>
<221> mat_peptide
<222> (120)..(1295)

```

```

<400> 3
gggaacgtag aactctccaa caataaatac atttgataag aaag atg gct tta aaa 56
                                         Met Ala Leu Lys
                                         -25

```

```

gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta 104
Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu
-20 -15 -10

```

```

ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga gac tgt aga cag 152
Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly Asp Cys Arg Gln
-5 -1 1 5 10

```

```

caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc tgc aac cag tgt 200
Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro Cys Asn Gln Cys
15 20 25

```

```

ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc ggc tat ggg gag 248
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
30 35 40

```

```

gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc aag gag gac tgg 296
Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp
45 50 55

```

```

ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca gtg gtg aac cgc 344
Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg
60 65 70 75

```

```

ttt cag aag gca aat tgt tca gcc acc agt gat gcc atc tgc ggg gac 392
(3/16)

```

Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	Ile	Cys	Gly	Asp	
				80					85					90		
tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	ggc	ttt	caa	gac	440
Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	Gly	Phe	Gln	Asp	
			95					100				105				
atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	tac	gaa	ccg	cac	488
Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	Tyr	Glu	Pro	His	
		110				115						120				
tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	acg	gcc	tcc	agc	536
Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	Thr	Ala	Ser	Ser	
	125					130					135					
cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	gct	ctg	gcc	acc	584
Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	Ala	Leu	Ala	Thr	
140					145					150					155	
gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	tgt	aag	aga	cag	632
Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	Cys	Lys	Arg	Gln	
				160					165					170		
ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	cag	gac	att	cag	680
Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	Gln	Asp	Ile	Gln	
			175					180					185			
tac	aac	ggc	tct	gag	ctg	tcg	tgt	ctt	gac	aga	cct	cag	ctc	cac	gaa	728
Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	Gln	Leu	His	Glu	
		190					195					200				
tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	tca	gtg	cag	acc	776
Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	Ser	Val	Gln	Thr	
	205				210						215					
tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	gag	gag	gcc	tgc	824
Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	Glu	Glu	Ala	Cys	
220					225					230					235	
agc	ccc	aac	ccg	gcg	act	ctt	ggc	tgt	ggg	gtg	cat	tct	gca	gcc	agt	872
Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	Ser	Ala	Ala	Ser	
				240					245					250		
ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	gtg	ccg	act	ttc	920
Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	Val	Pro	Thr	Phe	
			255					260					265			
ttc	gga	tcc	ctc	acg	cag	tcc	atc	tgt	ggc	gag	ttt	tca	gat	gcc	tgg	968
Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	Ser	Asp	Ala	Trp	
		270					275					280				
cct	ctg	atg	cag	aat	ccc	atg	ggc	ggc	gac	aac	atc	tct	ttt	tgt	gac	1016
Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	Ser	Phe	Cys	Asp	
	285					290					295					
tct	tat	cct	gaa	ctc	act	gga	gaa	gac	att	cat	tct	ctc	aat	cca	gaa	1064
Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser	Leu	Asn	Pro	Glu	
300					305					310					315	
ctt	gaa	agc	tca	acg	tct	ttg	gat	tca	aat	agc	agt	caa	gat	ttg	gtt	1112
Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	Gln	Asp	Leu	Val	
				320					325					330		
ggc	ggg	gct	gtt	cca	gtc	cag	tct	cat	tct	gaa	aac	ttt	aca	gca	gct	1160

Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	Phe	Thr	Ala	Ala		
			335					340					345				
act	gat	tta	tct	aga	tat	aac	aac	aca	ctg	gta	gaa	tca	gca	tca	act		1208
Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu	Ser	Ala	Ser	Thr		
		350					355					360					
cag	gat	gca	cta	act	atg	aga	agc	cag	cta	gat	cag	gag	agt	ggc	gct		1256
Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln	Glu	Ser	Gly	Ala		
	365					370					375						
atc	atc	cac	cca	gcc	act	cag	acg	tcc	ctc	cag	gaa	gct	taa	aga	ac		1305
Ile	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Glu	Ala					
380					385					390							
gcttctttct	gcagtagaag	cgtgtgctgg	aacccaaaga	gtactccttt	gttaggctta												1365
tggactgagc	agtctggacc	ttgcatggct	tctggggcaa	aaataaatct	gaaccaaact												1425
gacggcattt	gaagcctttc	agccagttgc	ttctgagcca	gaccagctgt	aagctgaaac												1485
ctcaatgaat	aacaagaaaa	gactccaggc	cgactcatga	tactctgcat	ctttcctaca												1545
tgagaagctt	ctctgccaca	aaagtgactt	caaagacgga	tgggttgagc	tggcagccta												1605
tgagattgtg	gacatataac	aagaaacaga	aatgccctca	tgcttatttt	catggtgatt												1665
gtgggttttac	aagactgaag	accagagta	tactttttc														1704

<210> 4  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Origin: human bone marrow stromal cell line HAS303

<400> 4

Met	Ala	Leu	Lys	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu		
-25					-20					-15					-10		

Leu	Val	Leu	Leu	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Thr	Gly		
				-5				-1	1				5				

Asp	Cys	Arg	Gln	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro		
		10					15					20					

Cys	Asn	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe		
25						30					35						

Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe		
40					45					50					55		

Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala		
				60					65					70			

(5/16)

Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala  
 75 80 85  
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
 90 95 100  
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
 105 110 115  
 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser  
 120 125 130 135  
 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser  
 140 145 150  
 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr  
 155 160 165  
 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser  
 170 175 180  
 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro  
 185 190 195  
 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp  
 200 205 210 215  
 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys  
 220 225 230  
 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His  
 235 240 245  
 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met  
 250 255 260  
 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe  
 265 270 275  
 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile  
 280 285 290 295  
 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser  
 300 305 310  
 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser  
 315 320 325



Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn  
330 335 340

Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu  
345 350 355

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln  
360 365 370 375

Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu  
380 385 390

Ala

<210> 5  
<211> 1269  
<212> DNA  
<213> Homo sapiens

<400> 5  
atggcctttaa aagtgtact agaacaagag aaaacgtttt tcactctttt agtattacta 60  
ggctattttgt catgtaaagt gacttgtgaa acaggagact gtagacagca agaattcagg 120  
gatcggctctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag 180  
gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggtc 240  
aaggaggact ggggcttcca gaaatgcaag ccctgtcttg actgcgcagt ggtgaaccgc 300  
tttcagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga 360  
ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac 420  
cctcctcctc cttacgaacc gcactgtgcc agcaagggtca acctcgtgaa gatcgcgtcc 480  
acggcctcca gcccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc 540  
gtcctgtctg ccctgtcat cctctgtgtc atctattgta agagacagtt tatggagaag 600  
aaaccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt 660  
cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac 720  
tcagtgcaga cctgcgggcc ggtgcgcttg ctcccatcca tgtgtgtgta ggaggcctgc 780  
agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga 840  
aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc 900  
tgtggcgagt tttcagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc 960  
tctttttgtg actcttatcc tgaactcact ggagaagaca ttcattctct caatccagaa 1020  
cttgaaagct caacgtcttt ggattcaaata agcagtcaag atttggttgg tggggctgtt 1080

(7/16)

ccagtccagt ctcattctga aaactttaca gcagctactg atttatctag atataacaac	1140
acactggttag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag	1200
gagagtggcg ctatcatcca cccagccact cagacgtccc tccaggtaag gcagcgactg	1260
ggttccctg	1269

<210> 6  
 <211> 1496  
 <212> DNA  
 <213> Homo sapiens

<400> 6	
gggaacgtag aactctccaa caataaatac atttgataag aaagatggct ttaaaagtgc	60
tactagaaca agagaaaacg tttttcactc ttttagtatt actaggctat ttgtcatgta	120
aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact	180
gtgttccctg caaccagtgt gggccaggca tggagtgtgc taaggaatgt ggcttcggct	240
atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct	300
tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt	360
gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga	420
aacttgctcg ctttcaagac atggagtgtg tgccttgtag agaccctcct cctccttacg	480
aaccgcactg tgccagcaag gtcaacctcg tgaagatcgc gtccacggcc tccagcccac	540
gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc	600
tcatectctg tgtcatctat tgtaagagac agtttatgga gaagaaaccc agctgggtctc	660
tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc	720
tccacgaata tgcccacaga gcctgctgcc agtgccgccg tgactcagtg cagacctgcg	780
ggccggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aaccggcgga	840
ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg	900
gggagatggt gccgactttc ttcggatccc tcacgcagtc catctgtggc gagttttcag	960
atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt	1020
atcctgaact cactggagaa gacattcatt ctctcaatcc agaacttgaa agctcaacgt	1080
ctttggattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt	1140
ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag	1200
catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca	1260
tccacccagc cactcagacg tccctccagg taaggcagcg actgggttcc ctgtgaacac	1320
agcactgact tacagtagat cagaactctg ttcccagcat aagatttggg ggaacctgat	1380
gagttttttt tttgcatctt taataatttc ttgtatgttg tagagtatgt tttaaataa	1440



atttcaagta ttttttttaa aaactaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1496

<210> 7  
 <211> 1496  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Origin: human bone marrow stromal cell line HAS303

<220>  
 <221> CDS  
 <222> (45)..(1313)

<220>  
 <221> sig\_peptide  
 <222> (45)..(119)

<220>  
 <221> mat\_peptide  
 <222> (120)..()

<400> 7  
 gggaacgtag aactctccaa caataaatac atttgataag aaag atg gct tta aaa 56  
 Met Ala Leu Lys  
 -25

gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta 104  
 Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu  
 -20 -15 -10

ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga gac tgt aga cag 152  
 Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly Asp Cys Arg Gln  
 -5 -1 1 5 10

caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc tgc aac cag tgt 200  
 Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro Cys Asn Gln Cys  
 15 20 25

ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc ggc tat ggg gag 248  
 Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu  
 30 35 40

gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc aag gag gac tgg 296  
 Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp  
 45 50 55

ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca gtg gtg aac cgc 344  
 Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg  
 60 65 70 75

ttt cag aag gca aat tgt tca gcc acc agt gat gcc atc tgc ggg gac 392  
 Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala Ile Cys Gly Asp  
 80 85 90

tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc ggc ttt caa gac 440  
 Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp  
 95 100 105

atg gag tgt gtg cct tgt gga gac cct cct cct cct tac gaa ccg cac Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His 110 115 120	488
tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc acg gcc tcc agc Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser Thr Ala Ser Ser 125 130 135	536
cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc gct ctg gcc acc Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr 140 145 150 155	584
gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat tgt aag aga cag Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg Gln 160 165 170	632
ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca cag gac att cag Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln 175 180 185	680
tac aac ggc tct gag ctg tcg tgt ctt gac aga cct cag ctc cac gaa Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu 190 195 200	728
tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac tca gtg cag acc Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp Ser Val Gln Thr 205 210 215	776
tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt gag gag gcc tgc Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys Glu Glu Ala Cys 220 225 230 235	824
agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser 240 245 250	872
ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe 255 260 265	920
ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp 270 275 280	968
cct ctg atg cag aat ccc atg ggt ggt gac aac atc tct ttt tgt gac Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp 285 290 295	1016
tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu 300 305 310 315	1064
ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val 320 325 330	1112
ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala 335 340 345	1160
act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr 350 355 360	1208

cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct	1256
Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala	
365 370 375	

atc atc cac cca gcc act cag acg tcc ctc cag gta agg cag cga ctg	1304
Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val Arg Gln Arg Leu	
380 385 390 395	

ggg tcc ctg tgaacacagc actgacttac agtagatcag aactctgttc	1353
Gly Ser Leu	

ccagcataag atttggggga acctgatgag tttttttttt gcatcttttaa taatttcttg	1413
--	------

tatgttgtag agtatgtttt aaaataaatt tcaagtattt tttttaaaaa ctaaaaaaaaa	1473
--	------

aaaaaaaaaa aaaaaaaaaa aaa	1496
---------------------------	------

<210> 8  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Origin: human bone marrow stromal cell line HAS303

<400> 8

Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
-25 -20 -15 -10

Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
-5 -1 1 5

Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
10 15 20

Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
25 30 35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
40 45 50 55

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
60 65 70

Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
75 80 85

Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
90 95 100

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
(11/16)

105

110

115

Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser  
 120 125 130 135

Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser  
 140 145 150

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr  
 155 160 165

Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser  
 170 175 180

Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro  
 185 190 195

Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp  
 200 205 210 215

Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys  
 220 225 230

Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His  
 235 240 245

Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met  
 250 255 260

Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe  
 265 270 275

Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile  
 280 285 290 295

Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser  
 300 305 310

Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser  
 315 320 325

Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn  
 330 335 340

Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu  
 345 350 355

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln  
 (12/16)

360		365		370		375
Glu	Ser	Gly	Ala	Ile	Ile	His
				380		
				Pro	Ala	Thr
				385		
				Gln	Thr	Ser
						Leu
						Gln
						390
						Val

Arg Gln Arg Leu Gly Ser Leu  
395

<210> 9  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<220>  
 <221> misc\_feature  
 <222> 27..35  
 <223> n can be any nucleotide

<400> 9  
 cgattgaatt ctagacctgc ctcgagnnnn nnnnn 35

<210> 10  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer OAF065

<400> 10  
 agaaagatgg ctttaaaagt gctactag 28

<210> 11  
 <211> 122  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Aminod acid sequence of OAF065s

<400> 11  
 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu  
 1 5 10 15  
 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly  
 20 25 30  
 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro  
 35 40 45  
 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
 50 55 60

Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe  
 65 70 75 80  
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala  
 85 90 95  
 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala  
 100 105 110  
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr  
 115 120

<210> 12  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30  
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110  
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125  
 Lys Asn Gln Tyr  
 130

<210> 13  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
 1 5 10 15  
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30  
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45



Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60  
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80  
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95  
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110  
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr  
 115 120 125

<210> 14  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
 1 5 10 15  
 Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
 20 25 30  
 Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
 35 40 45  
 Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
 50 55 60  
 Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr  
 65 70 75 80  
 Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser  
 85 90 95  
 Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly  
 100 105 110  
 Tyr Tyr

<210> 15  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 1 5 10 15  
 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 20 25 30  
 Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60  
 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80  
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95  
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 100 105 110  
 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 115 120 125  
 Cys Lys Pro Asn Phe Phe  
 130